

# SEQUENCE LISTING

<110> CuraGen Corporation et al.  
 Alsobrook II, John P.  
 Eichen, Joseph  
 Lepley, Denise M.  
 Miller, Charles E.  
 Mezes, Peter

<120> COMPOSITIONS AND METHODS OF USE FOR A FIBROBLAST GROWTH FACTOR

<130> 15966-557 SNP NATL (Cura-57 SNP NATL)

<140> 10.578,234

<141> 2004-11-03

<150> 10/702,126

<151> 2003-11-04

<160> 24

<170> CuraSeqList version 0.1

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<220>

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Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala	
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cgc ggc ggg ccg ggg gct gcg cag ctg gcg cac ctg cac ggc atc ctg	192
Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu	
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cgc cgc ccg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg	240
Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu	
65 70 75 80	

ccc gac ggc agc gtg cag ggc acc ccg cag gac cac agc ctc ttc ggt	288
Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly	
85 90 95	

atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt	336
Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly	
100 105 110	

gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat	384
Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr	
115 120 125	
gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa	432
Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu	
130 135 140	
gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac	480
Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp	
145 150 155 160	
act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act cca aga	528
Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg	
165 170 175	
gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct	576
Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro	
180 185 190	
aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag aac cta ctg	624
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Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu	
65 70 75 80	
Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly	
85 90 95	
Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly	
100 105 110	
Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr	
115 120 125	
Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu	
130 135 140	

Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp  
 145 150 155 160  
 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg  
 165 170 175  
 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro  
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 Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu  
 195 200 205  
 Met Tyr Thr  
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 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala  
 35 40 45  
 cgc ggc ggg ccg ggg gct gcg cag ctg gcg cac ctg cac ggc atc ctg 192  
 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu  
 50 55 60  
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 65 70 75 80  
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 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly  
 85 90 95  
 atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt 336  
 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly  
 100 105 110  
 gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat 384  
 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr  
 115 120 125  
 gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa 432  
 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu  
 130 135 140

gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac 480  
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 145 150 155 160

act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act cca aga 528  
 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg  
 165 170 175

gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct 576  
 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro  
 180 185 190

aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag gac cta ctg 624  
 Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu  
 195 200 205

atg tac act 633  
 Met Tyr Thr  
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Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala  
 35 40 45

Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu  
 50 55 60

Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu  
 65 70 75 80

Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly  
 85 90 95

Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly  
 100 105 110

Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr  
 115 120 125

Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu  
 130 135 140

Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp  
 145 150 155 160

Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg  
 165 170 175

Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro  
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Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu  
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Met Tyr Thr  
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 tac tgc cgt act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt 96  
 Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val  
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 cag ggt acc cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc 144  
 Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile  
 35 40 45  
 tct gtt gct gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg 192  
 Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu  
 50 55 60  
 tac ctg ggt atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg 240  
 Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu  
 65 70 75 80  
 acc tct gaa tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac 288  
 Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn  
 85 90 95  
 acc tac tct tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac 336  
 Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr  
 100 105 110  
 ttc gtt gct ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct 384  
 Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser  
 115 120 125  
 aaa cgt cac cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg 432  
 Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro  
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 gag cgt gtt cca gaa ctg tat aaa aac ctg ctg atg tac acc taa 477  
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Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile  
35 40 45

Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu  
50 55 60

Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu  
65 70 75 80

Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn  
85 90 95

Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr  
100 105 110

Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser  
115 120 125

Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro  
130 135 140

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ttg ggc cag ccg ggg gca gcg cag ctg gcg cac ctg cac ggc atc ctg 96  
Leu Gly Gln Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu  
20 25 30

cgc cgc cgg cag ctc tat tgc cgc acc ggc ttc cac ctg cag atc ctg 144  
Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu  
35 40 45

ccc gac ggc agc gcg cag ggc acc cgg cag gac cac agc ctc ttc ggt 192  
Pro Asp Gly Ser Ala Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly  
50 55 60

atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att aga ggt 240  
Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly  
65 70 75 80

gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa ctc tat	288
Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr	
85 90 95	
gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag ttt gaa	336
Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu	
100 105 110	
gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat gga gac	384
Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp	
115 120 125	
act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act cca aga	432
Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg	
130 135 140	
gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc tta cct	480
Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro	
145 150 155 160	
aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag aac cta ctg	528
Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu	
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atg tac act tag	540
Met Tyr Thr	

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Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu	
35 40 45	
Pro Asp Gly Ser Ala Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly	
50 55 60	
Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly	
65 70 75 80	
Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr	
85 90 95	
Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu	
100 105 110	
Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp	
115 120 125	
Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg	
130 135 140	

Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro  
 145 150 155 160

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 165 170 175

Met Tyr Thr

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 ccggatgggt ctgttcaggg taccgcgtcag gaccactctc tggtcgggtat cctggaattc 300  
 atctctgttg ctgttggtct ggtttctatc cgtgggtgtg actctggcct gtacctgggt 360  
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 gaacagtttg aagagaactg gtacaacacc tactcttcca acatctacaa acatgggtgac 480  
 accggccgtc gctacttctg tgctctgaac aaagacggta ccccgcgta tgggtgctcgt 540  
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 tctaacatat ataaacatgg agacactggc cgcagggtatt ttgtggcact taacaaagac 420  
 ggaactccaa gagatggcgc caggtccaag aggcattcaga aatttacaca tttcttacct 480  
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 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu  
 35 40 45  
 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly  
 50 55 60



Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly  
65 70 75 80

Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr  
85 90 95

Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu  
100 105 110

Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp  
115 120 125

Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg  
130 135 140

Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro  
145 150 155 160

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165 170 175

Met Tyr Thr

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1 5 10 15

cag cag gtt ggt tct cac ttc ctg ctg ccg ccg gct ggt gaa cgt ccg 96  
Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro  
20 25 30

cca ctg ctg ggt gaa cgt cgc tcc gca gct gaa cgc tcc gct cgt ggt 144  
Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly  
35 40 45

ggc ccg ggt gct gct cag ctg gct cac ctg cat ggt atc ctg cgt cgc 192  
Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu Arg Arg  
50 55 60

cgt cag ctg tac tgc cgt act ggt ttc cac ctg cag atc ctg ccg gat 240  
Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp  
65 70 75 80

ggt tct gtt cag ggt acc cgt cag gac cac tct ctg ttc ggt atc ctg 288  
Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu  
85 90 95

gaa ttc atc tct gtt gct gtt ggt ctg gtt tct atc cgt ggt gtt gac 336  
Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp

100	105	110	
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Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser			
115	120	125	
gaa aaa ctg acc tct gaa tgc atc ttc cgt gaa cag ttt gaa gag aac			432
Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn			
130	135	140	
tgg tac aac acc tac tct tcc aac atc tac aaa cat ggt gac acc ggc			480
Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly			
145	150	155	160
cgt cgc tac ttc gtt gct ctg aac aaa gac ggt acc ccg cgt gat ggt			528
Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly			
165	170	175	
gct cgt tct aaa cgt cac cag aaa ttc acc cac ttc ctg ccg cgc cca			576
Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro			
180	185	190	
gtt gac ccg gag cgt gtt cca gaa ctg tat aaa aac ctg ctg atg tac			624
Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr			
195	200	205	
acc taa			630
Thr			

<210> 13  
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 Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly  
 35 40 45  
 Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu Arg Arg  
 50 55 60  
 Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp  
 65 70 75 80  
 Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu  
 85 90 95  
 Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp  
 100 105 110  
 Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser  
 115 120 125  
 Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn

130	135	140
Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly		
145	150	155 160
Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly		
	165	170 175
Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro		
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Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr		
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1 5 10 15	
ttc ctg ctg ccg ccg gct ggt gaa cgt ccg cca ctg ctg ggt gaa cgt	96
Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg	
20 25 30	
cgc tcc gca gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct cag	144
Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln	
35 40 45	
ctg gct cac ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc cgt	192
Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg	
50 55 60	
act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt acc	240
Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr	
65 70 75 80	
cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt gct	288
Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala	
85 90 95	
gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg ggt	336
Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly	
100 105 110	
atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct gaa	384
Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu	
115 120 125	
tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac acc tac tct	432
Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser	

130	135	140	
tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt gct			480
Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala			
145	150	155	160
ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt cac			528
Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His			
	165	170	175
cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt gtt			576
Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val			
	180	185	190
cca gaa ctg tat aaa aac ctg ctg atg tac acc taa			612
Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr			
	195	200	

<210> 15

<211> 203

<212> PRT

<213> Homo sapiens

<400> 15

Gly Phe Leu Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His
1 5 10 15

Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg
20 25 30

Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln
35 40 45

Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg
50 55 60

Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr
65 70 75 80

Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala
85 90 95

Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly
100 105 110

Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu
115 120 125

Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser
130 135 140

Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala
145 150 155 160

Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His
165 170 175

Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val
180 185 190

Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr

195

200

<210> 16  
 <211> 603  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(600)

<400> 16

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ggc ggt ctg gag ggt ctg ggt cag cag gtt ggt tct cac ttc ctg ctg      48
Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu
  1              5              10              15

ccg ccg gct ggt gaa cgt ccg cca ctg ctg ggt gaa cgt cgc tcc gca      96
Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala
              20              25              30

gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct cag ctg gct cac     144
Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His
              35              40              45

ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc cgt act ggt ttc     192
Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe
              50              55              60

cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt acc cgt cag gac     240
His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp
              65              70              75              80

cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt gct gtt ggt ctg     288
His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu
              85              90              95

gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg ggt atg aac gac     336
Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp
              100             105             110

aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct gaa tgc atc ttc     384
Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe
              115             120             125

cgt gaa cag ttt gaa gag aac tgg tac aac acc tac tct tcc aac atc     432
Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile
              130             135             140

tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt gct ctg aac aaa     480
Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys
              145             150             155             160

gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt cac cag aaa ttc     528
Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe
              165             170             175

acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt gtt cca gaa ctg     576
Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu
              180             185             190

tat aaa aac ctg ctg atg tac acc taa                                603

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Tyr Lys Asn Leu Leu Met Tyr Thr  
 195 200

<210> 17  
 <211> 200  
 <212> PRT  
 <213> Homo sapiens

<400> 17  
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 Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala  
 20 25 30  
 Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His  
 35 40 45  
 Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe  
 50 55 60  
 His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp  
 65 70 75 80  
 His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu  
 85 90 95  
 Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp  
 100 105 110  
 Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe  
 115 120 125  
 Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile  
 130 135 140  
 Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys  
 145 150 155 160  
 Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe  
 165 170 175  
 Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu  
 180 185 190  
 Tyr Lys Asn Leu Leu Met Tyr Thr  
 195 200

<210> 18  
 <211> 594  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(591)

<400> 18  
 gag ggt ctg ggt cag cag gtt ggt tct cac ttc ctg ctg ccg ccg gct 48  
 Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala  
 1 5 10 15

ggt gaa cgt ccg cca ctg ctg ggt gaa cgt cgc tcc gca gct gaa cgc	96
Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg	
20 25 30	
tcc gct cgt ggt ggc ccg ggt gct gct cag ctg gct cac ctg cat ggt	144
Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly	
35 40 45	
atc ctg cgt cgc cgt cag ctg tac tgc cgt act ggt ttc cac ctg cag	192
Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln	
50 55 60	
atc ctg ccg gat ggt tct gtt cag ggt acc cgt cag gac cac tct ctg	240
Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu	
65 70 75 80	
ttc ggt atc ctg gaa ttc atc tct gtt gct gtt ggt ctg gtt tct atc	288
Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile	
85 90 95	
cgt ggt gtt gac tct ggc ctg tac ctg ggt atg aac gac aaa ggc gaa	336
Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu	
100 105 110	
ctg tac ggt tct gaa aaa ctg acc tct gaa tgc atc ttc cgt gaa cag	384
Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln	
115 120 125	
ttt gaa gag aac tgg tac aac acc tac tct tcc aac atc tac aaa cat	432
Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His	
130 135 140	
ggt gac acc ggc cgt cgc tac ttc gtt gct ctg aac aaa gac ggt acc	480
Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr	
145 150 155 160	
ccg cgt gat ggt gct cgt tct aaa cgt cac cag aaa ttc acc cac ttc	528
Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe	
165 170 175	
ctg ccg cgc cca gtt gac ccg gag cgt gtt cca gaa ctg tat aaa aac	576
Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn	
180 185 190	
ctg ctg atg tac acc taa	594
Leu Leu Met Tyr Thr	
195	
<210> 19	
<211> 197	
<212> PRT	
<213> Homo sapiens	
<400> 19	
Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala	
1 5 10 15	
Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg	
20 25 30	

Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly  
           35                          40                          45  
 Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln  
       50                          55                          60  
 Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu  
       65                          70                          75                          80  
 Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile  
           85                          90                          95  
 Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu  
           100                          105                          110  
 Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln  
       115                          120                          125  
 Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His  
       130                          135                          140  
 Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr  
       145                          150                          155                          160  
 Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe  
           165                          170                          175  
 Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn  
           180                          185                          190  
 Leu Leu Met Tyr Thr  
       195

<210> 20  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(564)

<400> 20  
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 His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu  
       1                          5                          10                          15  
 cgt cgc tcc gca gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct 96  
 Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala  
           20                          25                          30  
 cag ctg gct cac ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc 144  
 Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys  
           35                          40                          45  
 cgt act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt 192  
 Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly  
       50                          55                          60  
 acc cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt 240  
 Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val



65	70	75	80	
gct gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg				288
Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu	85	90	95	
ggt atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct				336
Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser	100	105	110	
gaa tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac acc tac				384
Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr	115	120	125	
tct tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt				432
Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val	130	135	140	
gct ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt				480
Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg	145	150	155	160
cac cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt				528
His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg	165	170	175	
gtt cca gaa ctg tat aaa aac ctg ctg atg tac acc taa				567
Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr	180	185		

<210> 21

<211> 188

<212> PRT

<213> Homo sapiens

<400> 21

His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu				
1	5	10	15	
Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala	20	25	30	
Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys	35	40	45	
Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly	50	55	60	
Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val	65	70	75	80
Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu	85	90	95	
Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser	100	105	110	
Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr	115	120	125	
Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val				

130 135 140

Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg  
 145 150 155 160

His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg  
 165 170 175

Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr  
 180 185

<210> 22  
 <211> 447  
 <212> DNA  
 <213> Homo sapiens

<400> 22  
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 gtggcagtg gactggtcag tattagaggt gtggacagtg gtctctatct tggaatgaat 180  
 gacaaaggag aactctatgg atcagagaaa cttacttccg aatgcatctt tagggagcag 240  
 tttgaagaga actggtataa cacctattca tctaacatat ataaacatgg agacactggc 300  
 cgcaggtatt ttgtggcact taacaaagac ggaactccaa gagatggcgc caggtccaag 360  
 aggcacaga aatttacaca tttcttacct agaccagtgg atccagaaaa agttccagaa 420  
 ttgtacaagg acctactgat gtacact 447

<210> 23  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln  
 1 5 10 15

Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu  
 20 25 30

Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile  
 35 40 45

Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu  
 50 55 60

Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln  
 65 70 75 80

Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His  
 85 90 95

Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr  
 100 105 110

Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe  
 115 120 125

Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn  
 130 135 140

Leu Leu Met Tyr Thr  
 145

<210> 24  
 <211> 537  
 <212> DNA  
 <213> Homo sapiens

<400> 24  
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 ggggcagcgc agctggcgca cctgcacggc atcctgcgcc gccggcagct ctattgccgc 120  
 accggcttcc acctgcagat cctgcccgac ggcagcgtgc agggcacccg gcaggaccac 180  
 agcctcttcg gtatcttgga attcatcagt gtggcagtgg gactggtcag tattagaggt 240  
 gtggacagtg gtctctatct tggaatgaat gacaaaggag aactctatgg atcagagaaa 300  
 cttacttccg aatgcatctt tagggagcag tttgaagaga actggtataa cacctattca 360  
 tctaacatat ataaacatgg agacactggc cgcaggtatt ttgtggcact taacaaagac 420  
 ggaactccaa gagatggcgc caggtccaag aggcatacaga aatttacaca tttcttacct 480  
 agaccagtgg atccagaaag agttccagaa ttgtacaaga acctactgat gtacact 537